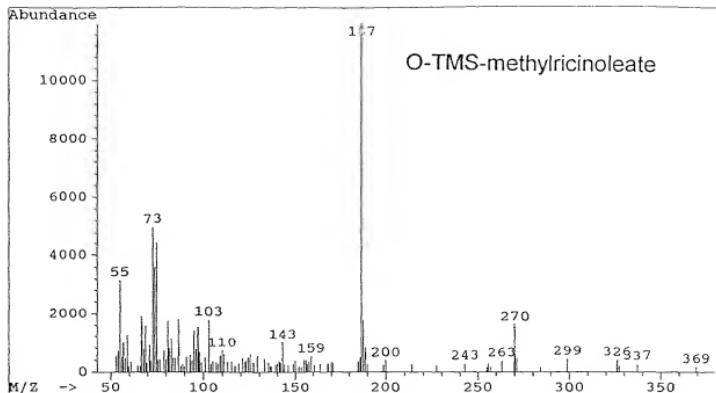
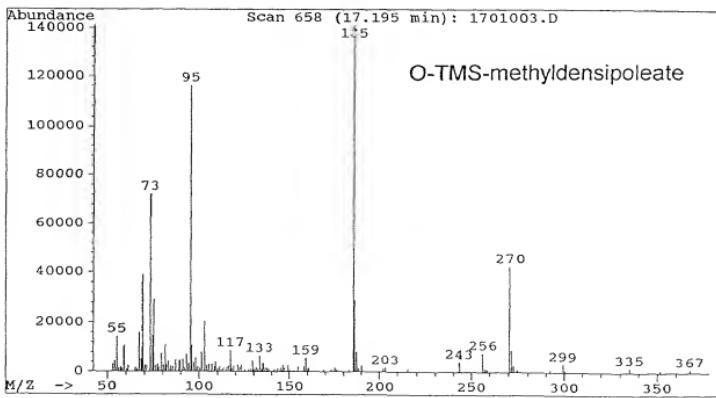


Figure 1A

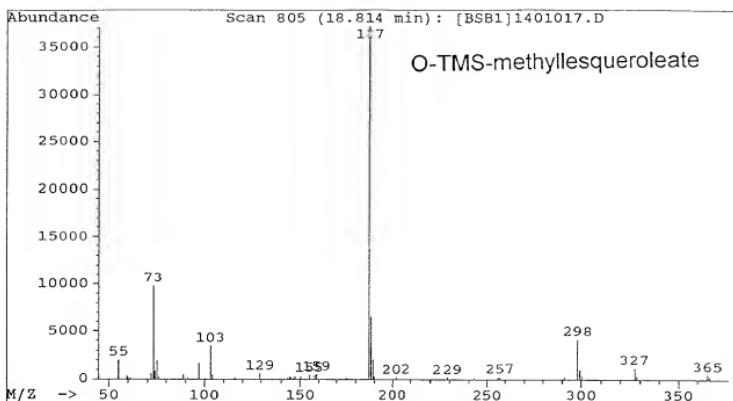


1B

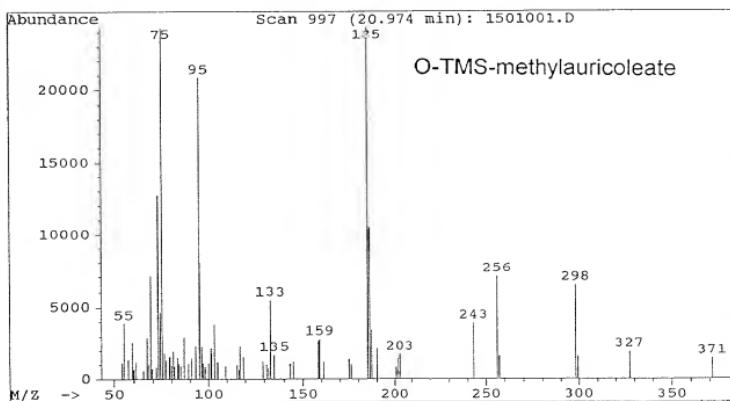


0101234567895432101

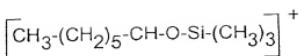
1C



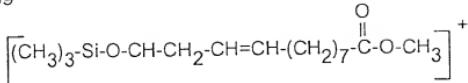
1D



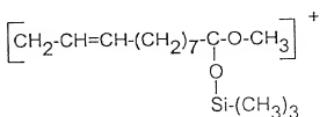
Ion #1: Mass 187



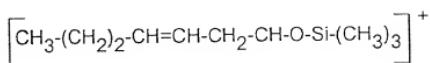
Ion #2: Mass 299



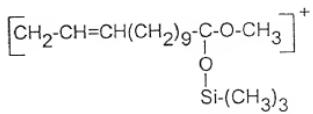
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of ion

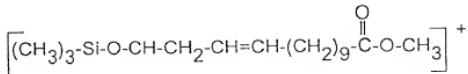
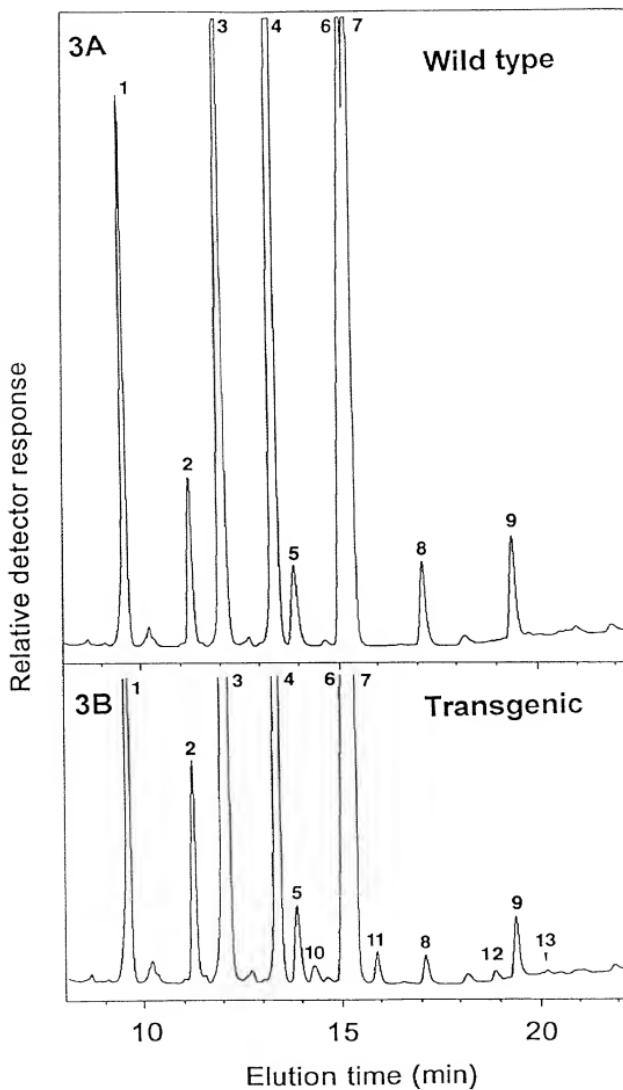


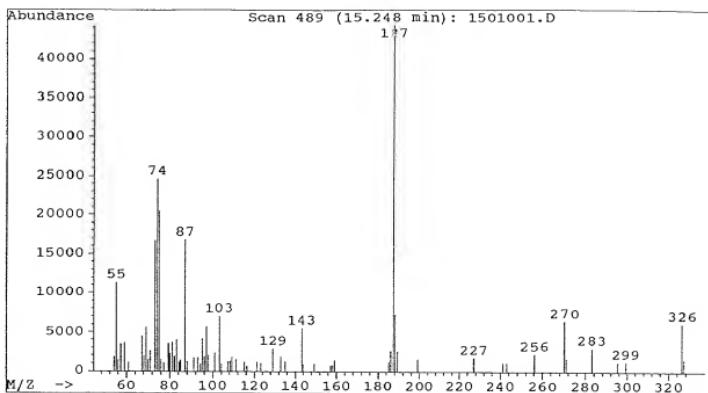
Figure 2

Figure 3

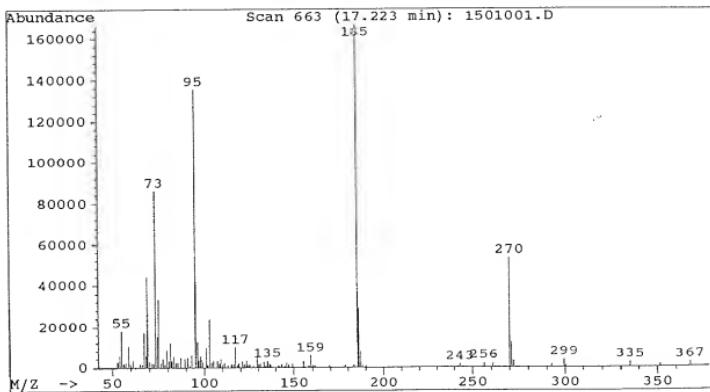


T0T290-68753360

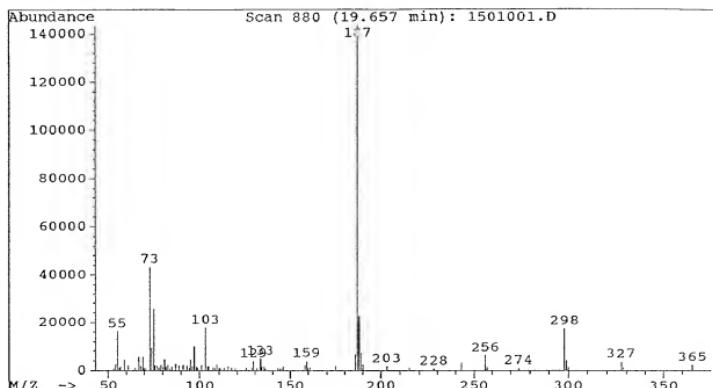
Figure 4A Mass spectrum of peak 10 from figure 3B



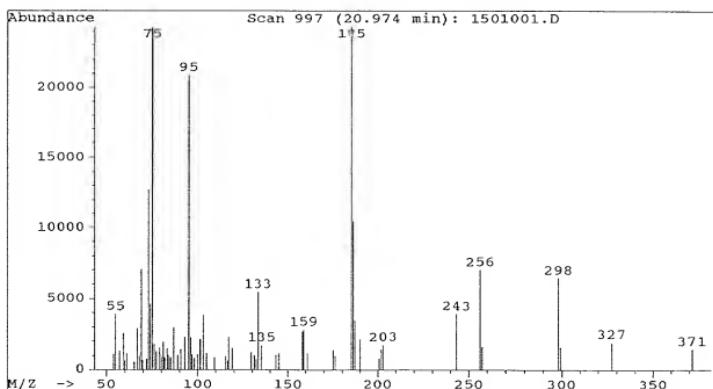
4B Mass spectrum of peak 11 from figure 3B



4C Mass spectrum of peak 12 from figure 3B



4D Mass spectrum of peak 13 from figure 3B



TATTGGCACC	10	GGCGGCACCA	20	TTCCAACAA	30	GGATCCCTAG	40	AAAAAGATGA	50	AGTCTTGTC	60
	70		80		90		100		110		120
CCACCTAAGA		AAGCTGCACT		CANATGGTAT		GTCAAATACC		TCAACAAACCC		TCTTGGACGC	
	130		140		150		160		170		180
ATTCTGGTGT		TAACAGTTCA		GTTTATCCTC		GGGTGGCCTT		TGTATCTAGC		CTTTAATGTA	
	190		200		210		220		230		240
TCAGGTAGAC		CTTATGATGG		TTTCGCTTCA		CATTCTTCC		CTCATGCACC		TATCTTAAG	
	250		260		270		280		290		300
GACCGTGAAC		GTCTCCAGAT		ATACATCTCA		GATGCTGGTA		TTCTAGCTGT		CTGTTATGGT	
	310		320		330		340		350		360
CTTTACCGTT		ACGCTGCTTC		ACAAGGATTG		ACTGCTATGA		TCTGCCTCTA		CGGAGTAGCC	
	370		380		390		400		410		420
CTTTTGATAG		TGAACTTTTT		CCTTGTCTTG		GTCACTTTCT		TGCAGCACAC		TCATCCTTCA	
	430		440		450		460		470		480
TTACCTCACT		ATGATTCAAC		CGAGTGGAA		TGGATTAGAG		GAGCTTTGGT		TACGGTAGAC	
	490		500		510		520		530		540
AGAGACTATG		GAATCTTGAA		CAAGGTGTTT		CACAACATAA		CAGACACCCA		CGTAGCACAC	
	550										
CAC											

Figure 5

10	20	30	40	50	60
TATAGGCACC	GGAGGCACCA	TTCCAACACA	GGATCCCTCG	AAAGAGATGA	AGTATTGTC
70	80	90	100	110	120
CCAAAGCAGA	AATCCGCAAT	CAAGTGGTAC	GGCGAACATCC	TCAACAAACCC	TCCTGGTCGC
130	140	150	160	170	180
ATCATGATGT	TAACGTGCA	GTTCGTCC	GGATGGCCT	TGTACTTAGC	CTTCAACGTT
190	200	210	220	230	240
TCTGGCAGAC	CCTACAATGG	TTTCGCTTCC	CATTTCTTCC	CCAATGCTCC	TATCTACAC
250	260	270	280	290	300
GACCGTGAAAC	GCCTCCAGAT	TTACATCTCT	GATGCTGGTA	TTCTAGCCGT	CTGTTATGGT
310	320	330	340	350	360
CTT TACCGTT	ACGCTGTTGC	ACAAGGACTA	GCCTCAATGA	TCTGTCTAAA	CGGAGTTCCG
370	380	390	400	410	420
CTTCTGATAG	TTAACTTTTT	CCTCGTCTTG	ATCACTTACT	TACAACACAC	TCACCCTCGG
430	440	450	460	470	480
TTGCCTCACT	ATGATTCA	AGAGTGGGAT	TGGCTTAGAG	GAGCTT	TACTGTAGAC
490	500	510	520	530	540
AGAGACTATG	GAATCTTGAA	CAAGGTGTT	CATAACATCA	CAGACACCCA	CGTCGCACAC
550					

CACT

101250-6815890

Figure 6

F0T290 " 68T588860



Figure 7

09885180-062101

AT GAA GCT TTA TAA GAA GTT AGT TTT CTC TGG TGA CAG AGA AAT TNT	47
GTC AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG	95
GTG NTG ATG CTG ATG TGG TGA TGT ATT CAT CAA ATA CTA AAT ACT	143
ACA TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT	191
TGG ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG	239
AAG AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC	287
TTC TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA	335
ATC TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT	383
Met Gly Ala Gly Gly Arg Ile Met Val Thr	10
CAG CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC	431
Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys	26
CCC TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT	479
Glu Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala Ile Pro Gln	42
GAG AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG	527
His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr	58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA	575
Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe	74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC	623
Ser Leu Leu Pro Gin Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr	90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT	671
Trp Val Cys Gin Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His	106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT	719
Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr	122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT	767
Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp	138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG	815
Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys	154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA	863
Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val	170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT	911
Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln	186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG	959

Figure 8A

05012018-05153800

Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg	202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA	1007
Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe	218
CCT TAT GAT GGT TTC GCT TCA CAT TTC CCT CAT GCA CCT ATC TTT	1055
Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu	234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA	1103
Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr	250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT TCA CAA GGA TTG ACT	1151
Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe	266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC	1199
Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His	282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT	1247
Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val	298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA	1295
Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp	314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC	1343
Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala	330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA	1391
Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His	346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC	1439
Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu	362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG	1487
Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr	378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC	1535
Tyr Tyr Asn Asn Lys Leu	384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT	1583
ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC	1631
TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT	1679
TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT	1727
GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG	1775
AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA	1823
AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG	1855

Figure 8B

09885189 - 0529101

		10	20	30	40	50		
LFFAH12	1	MGAGGRIM--	--VTPSSKKS	--ETEALKRG	PCEKPPFTVK	DLKKAIPQHC	50	
FAH12	1	MGGGGRMSTV	ITSNNSEKKG	--GSSHLCRA	PHTKPPFTLG	DLKRAIPPHC	50	
ATFAD2	1	MGAGGRMP--	--VPTSSKKS	--ETDTTKRV	PCEKPPFSVG	DLKKAIPPHC	50	
BNFAD2	1	MGAGGRMO--	--VSPPSKKS	--ETDNIKRV	PCTEPPFTVG	ELKKAIPPHC	50	
GMFA02-1	1	MGLA-KETTM	GGGRGVAKVE	VOGKKPLSRV	PNTKPPFTVG	QLKKAIPPHC	50	
GMFA02-2	1	MGAGGR----	TDVPPANRKS	--EVDPLRKV	PFEKPQFSLS	QIKKAIPPHC	50	
ZMFAD2	1	MGAGGRMTEK	EREKQEOLAR	ATGGAAMQRS	PVEKPPFTLG	QIKKAIPPHC	50	
RCFAD2	1	-----	-----	-----	-----	-----	50	
		60	70	80	90	100		
LFFAH12	51	FKRSIPIRSFS	YLLTIDITLVS	CFYYVATNYF	SLLPQPLSTY	LAPPLYWVCQ	100	
FAH12	51	FERSVFRSFS	YYAVDYLCSL	LFYSIATNPF	PYISSPPLS-Y	VAWLVYWLQ	100	
ATFAD2	51	FKRSIPIRSFS	YLI0DIIIAS	CFYYVATNYF	SLLPPLS-Y	LAPPLYWACQ	100	
BNFAD2	51	FKRSIPIRSFS	HLI0DIIIAS	CFYYVATTYF	PLLPNPLS-Y	FAPPLYWACQ	100	
GMFA02-1	51	FQRSLLTFS	YYVYDLSAF	IFY-IATTYF	HLLPQPOFS-L	IAWPVYVLO	100	
GMFA02-2	51	FORSVLRFS	YYVYDLTIAF	CLYYVATHYF	LILHPQLS-F	RGMAYWAVQ	100	
ZMFAD2	51	FERSVLSFS	YVYHDLVIAA	ALLYFALAI	PALPSPLR-Y	AAAPLYWIAQ	100	
RCFAD2	51	-----	-----	-----	-----	-----	100	
		110	120	130	140	150		
LFFAH12	101	GCVLTGIWVI	GHECGHHAFS	DYOWVDDTVG	FIFHSFLLVP	YFSWKYSHRR	150	
FAH12	101	GCLLTGWLVI	GHECGHHAFS	EYOLADDIV	LIVHSALLVP	YFSWKYSHRR	150	
ATFAD2	101	GCVLTGIWVI	AHECGHHAFS	DYOWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150	
BNFAD2	101	GCVLTGVWVI	AHECGHHAFS	DYOWLDDTVG	LIFHSFLLVP	YFSWKYSHRR	150	
GMFA02-1	101	GCLLTGVWVI	AHECGHHAFS	KYOWVDDVVG	LTLHSTLLVP	YFSWKYSHRR	150	
GMFA02-2	101	GCLLTGVWVI	AHECGHHAFS	DYOLLDDIVG	LILHSALLVP	YFSWKYSHRR	150	
ZMFAD2	101	G-----	-----AFS	DYS1LDDVVG	LVLHSSLVP	YFSWKYSHRR	150	
RCFAD2	101	-----	-----WVM	AHDGCHHAFS	DYOLLDDVVG	LILHSCLLPV	YFSWKHSHRR	150
		160	170	180	190	200		
LFFAH12	151	HHSNNGSLEK	DEVFVPPKKA	AVKWYKYKL-	NNPLGRILVL	TVOFILGWPL	200	
FAH12	151	HHSNIGSLER	DEVFPVPSKS	KISMWSKYS	NNPPGRVLT	AA TLLLGWPL	200	
ATFAD2	151	HHSNTGSLER	DEVFPVPKQS	AIKWYGYKL-	NNPLGRIMML	TVQFVLGWPL	200	
BNFAD2	151	HHSNTGSLER	DEVFPVPR-RS	GTSSGTAST-	STTFGRTVML	TVQFTLGWPL	200	
GMFA02-1	151	HHSNTGSLDR	DEVFPVPKPKS	KVAMFSKYL-	NNPLGRAVSL	LVTLTIGWPM	200	
GMFA02-2	151	HHSNTGSLER	DEVFPVPKQS	CIKWYSKYL-	NNPPGRVLT	AVTLLTGWPL	200	
ZMFAD2	151	HHSNTGSLER	DEVFPVPKKE	ALPWYTPYVY	NNPVGRVWHI	VVQLTLLGWPL	200	
RCFAD2	151	HHSNTGSLER	DEVFPVPKKS	SIRWYSKYL-	NNPPGRIMTI	AVTLSLGWPL	200	
		210	220	230	240	250		
LFFAH12	201	YLAFNVSGRP	YDG-FASHFF	PHAPIFKDRE	RLOIYISDAG	ILAVCYGLYR	250	
FAH12	201	YLAFNVSGRP	YDR-FACHYD	PYGPPIFSERE	RLOIYIADLG	IFATTFVLYQ	250	
ATFAD2	201	YLAFNVSGRP	YDG-FACHFF	PNAPIYNDRE	RLOIYISDAG	ILAVCFGGLYR	250	
BNFAD2	201	YLAFNVSGRP	YDGFACHFH	PNAPIYNDRE	RLOIYISDAG	ILAVCYGLLP	250	
GMFA02-1	201	YLAFNVSGRP	YDS-FASHYH	PYAPIYSNRE	RLLIYVSVA	LFSVTYSLYR	250	
GMFA02-2	201	YLALNVSGRP	YDR-FACHYD	PYGPIYSDRE	RLOIYISDAG	VLA VVYGLFR	250	
ZMFAD2	201	YLATNASGRP	YPR-FACHFD	PYGPIYNDRE	RAQIFVSDAG	VVA VAFGLYK	250	
RCFAD2	201	YLAFNVSGRP	YDR-FACHYD	PYGPIYNDRE	RIEIFISDAG	VLA VTFGLYQ	250	

Figure 9A

101290-6815860

		260	270	280	290	300	
LFFAH12	251	YAA\$QGLTAM	ICVYGVPLLI	VNFFFLVLVTF	LQHTHPSLPH	YDSTEWEMIR	300
FAH12	251	ATMAKGLAWV	MRIYGVPLLI	VNCFLVLMITY	LQHTHPAIPR	YGSSEWDWLR	300
ATFAD2	251	YAAAQGMASM	ICLYGVPLLI	VNAFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
BNFAD2	251	YAAVQGVASM	VCFLRVPLLI	VNGFLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
GMFAD2-1	251	VATLKGLWL	LCVYGVPLLI	VNGFLVTITY	LQHTHFALPH	YDSSEOWWLK	300
GMFAD2-2	251	LAMAKGLAWV	VCVYGVPLLV	VNGFLVLITF	LQHTHPALPH	YTSSSEWDWLR	300
ZMFAD2	251	LAAAFGVVMW	VRYYAVPLLI	VNAWLVLITY	LQHTHPSLPH	YDSSEWDWLR	300
RCFAD2	251	LAIKGLAWV	VCYVGVPLLV	VNSFLVLITF	LQHTHPALPH	YDSSEWDWLR	300
		310	320	330	340	350	
LFFAH12	301	GALTVDRDY	GILNKVFHN1	TDTVAHHLF	ATIPHNAME	ATEAIKPILG	350
FAH12	301	GAMTVDRDY	GVLNKVFHN1	ADTHVAHHLF	ATPVPHAME	ATKAIKPIMG	350
ATFAD2	301	GALATVDRDY	GILNKVFHN1	TDTVAHHLF	STMPHYNAME	ATKAIKPILG	350
BNFAD2	301	GALATVDRDY	GILNOGFHN1	TDTHEAHHLF	STMPHYHAME	ATKAIKPILG	350
GMFAD2-1	301	GALATMDRDY	GILNKVFHN1	TDTVAHHLF	STMPHYHAME	ATNAIKPILG	350
GMFAD2-2	301	GALATVDRDY	GILNKVFHN1	TDTVAHHLF	STMPHYHAME	ATKAIKPILG	350
ZMFAD2	301	GALATMDRDY	GILNRVFNH1	TDTVAHHLF	STMPHYHAME	ATKAIRPILG	350
RCFAD2	301	GALATVDRDY	GILNKVFHN1	TDTQVAHHLF	-----	-----	350
		360	370	380	390	400	
LFFAH12	351	DYYHFDGTPW	YYAMYREAKE	CLYVEPDTER	GKKGVYYYYNN	K-L.....	400
FAH12	351	EYYRYFDGTPF	YKALWREAKE	CLFVEPDEGA	PTQGVFWYRN	KY-.....	400
ATFAD2	351	DYYQFDGTPW	YYAMYREAKE	CIYVEPDREG	DKKGVYWMNN	K-L.....	400
BNFAD2	351	EYYQFDGTPW	VKAMWREAKE	CIYVEPDREG	EKKGVFWYNK	KL*.....	400
GMFAD2-1	351	EYYQFDGTPF	YKALWREAKE	CLYVEPDEGT	SEKGVYWMRN	KY-.....	400
GMFAD2-2	351	EYYRFDETTF	VKAMWREAKE	CIYVEPDOST	ESKGVFWYNK	KL-.....	400
ZMFAD2	351	DYYHFDPTPV	AKATWREAGE	CIYVEPE---	DRKGVFWYNK	KF*.....	400

Figure 9B

00000000000000000000000000000000

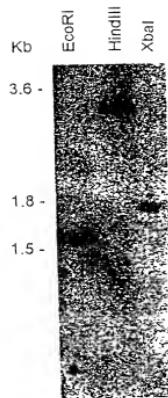
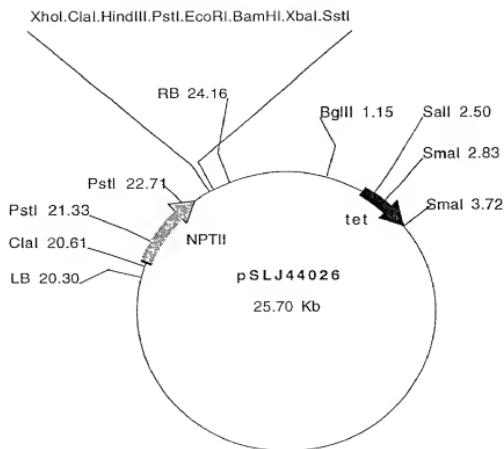


Figure 10

09885189 - 062101



Plasmid name: pSLJ44026

Plasmid size: 25.70 kb

Constructed by: Jonathon Jones

Construction date: 1992

Comments/References: Transgenic Research 1,285-297 (1992)

Figure 11

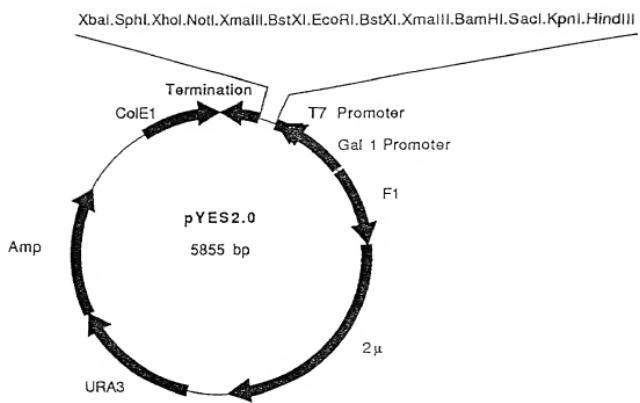


Figure 12

TOTALS: 698851802101

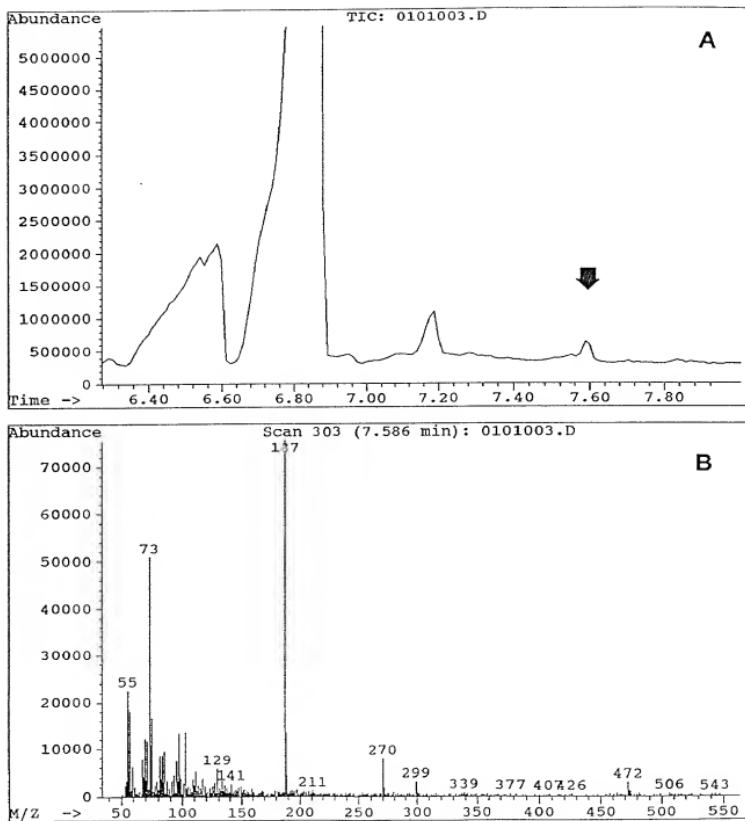


Figure 13